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Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒ A description of all covariates tested
☒	☐ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒ For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐ Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	The ELISA absorbance data was measured SPECTRAmax 250 (Molecular Devices) microplate reader. Characterization of glycosylation sites was performed on an UltiMate3000 nanoLC (Dionex) coupled with a hybrid triple quadrupole linear ion trap mass spectrometer, the 4000 Q Trap (SCIEX). MS data acquisition was performed using Analyst 1.6.1 software (SCIEX). For quantitative analysis of the glycoforms at the N297 site of IgG1, multiple-reaction monitoring (MRM) analysis for selected target glycopeptide was applied using the nanoLC-4000 Q Trap platform. All raw MRM data was processed using MultiQuant 2.1.1 (SCIEX). The binding affinity of IgGs from the various groups was determined by biolayer interferometry (BLI) using an OctetQK instrument (Pall ForteBio). Size exclusion chromatography was performed using AKTA pure on a Superdex-200 analytical gel filtration column and data was acquired on UNICORN 7 software (Cytiva). FACS and Cytokine data were acquired on Attune NxT flow cytometer (Invitrogen).
Data analysis	Octet data was analysed using ForteBio Data Analysis Software version 8.0.3.5. R statistical package version 1.2.1335 was used to generate the radar plots and perform multivariate linear regression analysis. FlowJo v10.6.2 was used to analyse the FACS and cytokine data. All other data were analyzed with GraphPad Prism 8.0. software. Biorender.com was used to generate the cartoon.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

All raw data are available from the corresponding author on reasonable request. Reference SARS-CoV-2 spike protein sequence was obtained from the NCBI database (https://www.ncbi.nlm.nih.gov/protein/1791269090).

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	No statistical sample size calculation was performed. Sample sizes for COVID-19 positive patient groups were determined based on availability of samples and associated clinical information from Kaiser Permanente Northern California across 17 counties in Northern California between March 30th-April 19th, 2020 or from Stanford Hospital (protocol #28205) or enrolled in the trial NCT04331899. 130 historical controls from multiple geographic locations and age groups were used as negative controls for establishing ELISA assay specificity. 1)Sera from 61 adult PCR positive COVID-19 patients, 802 children without a COVID-19 diagnosis, 130 historical negative controls and 12 subjects with documented seasonal coronavirus infections collected in early 2019 were screened for seropositivity. 2) Glycan analyses were done on IgG from 129 COVID-19 patients and 16 pediatric samples which were seropositive in our screen. 3)Sera from 38 individuals were randomly chosen from all the cohorts that represented the enitre range of fucosylation in the glycan analyses. 4) IgG was purified from sera of 13 COVID-19 patients with a range of anti-RBD IgG1 fucosylation 5)IgG was purified from sera of 8 COVID-19 patients with anti-RBD IgG1 fucosylation ranging from <80% -95% for immune complex mediated NK cell degranulation analysis.
Data exclusions	Samples were excluded from analysis if the patient was known to have received anti-inflammatory medications.
Replication	All the results were reliably reproduced and all replicate information are available in the figure legends.
Randomization	Samples were allocated to their groups based on their PCR status information and hospitalization status.
Blinding	Investigators were blinded to study subjects diagnoses during screening; COVID-19 patients and children were not known by investigators at the time of ELISA screening for RBD reactivity of serum or by investigators involved in relative quantitation of Fc glycoforms and IgG subclasses by mass spectrometry.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☐	☒ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☐	☒ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used

Mouse Anti-Human IgM-HRP- Southern Biotech, Cat. No- 9020-05 Lot No.- B2919-T719C
Goat Anti-Human IgA-HRP- Southern Biotech, Cat. No- 2050-05 Lot No.-J2416-Q999D
Goat Anti-Human IgG Fc-HRP- Southern Biotech, Cat. No.-2048-05 Lot No.-B0819-WH19B
Goat Anti-Human Ig Fab-HRP- Southern Biotech, Cat. No.-2085-05 Lot. No.-A4212-M616P
mAB 3022 (plasmid a gift from I. Wilson (The Scripps Research Institute) and produced in house, citation below)
Alexa Fluor 700 Anti-Human CD3 Antibody Clone OKT3 - BioLegend, Cat. No.-317340, Lot No.- B279661
Alexa Fluor 700 Anti-Human CD14 Antibody Clone 63D3 - BioLegend, Cat. No.-367114, Lot No.-B291968
APC Anti-Human CD11c Antibody Clone S-HCL-3 BioLegend, Cat. No.-371506, Lot No.- B263228
PE Anti-Human CD56 Antibody Clone 5.1H11 BioLegend, Cat. No.-362508 Lot No.- B269099
APC/Fire 750 Anti-Human HLA-DR Antibody Clone L243 BioLegend, Cat. No.-307658
Brilliant Violet 785 Anti-Human CD107a (LAMP-1) Antibody- BioLegend, Cat. No.-328644, Lot No.- B284309
Brilliant Violet 650 Anti-Human CD16 Antibody Clone 3G8- Biolegend, Cat. No.-302042, Lot.-B272554
Brilliant Violet 785 Anti-Human CD107a (LAMP-1) Antibody- BioLegend, Cat. No.-328644, Lot No.- B284309
Brilliant Violet 650 Anti-Human CD16 Antibody Clone 3G8- Biolegend, Cat. No.-302042, Lot.-B272554

Validation

For mAB3022: ter Meulen, J. et al. Human monoclonal antibody combination against SARS coronavirus: synergy and coverage of escape mutants. PLoS Med 3, e237 (2006).
All antibodies used for FACS and ELISAare well-established clones and commercially available. All antibodies were used at concentrations as recommended by the manufacturer and mentioned in the manuscript.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)

Expi293F™ Cells, Thermo Fisher Scientific (Catalog number: A14527)

Authentication

Non-authenticated

Mycoplasma contamination

Cell lines were not tested for Mycoplasma contamination

Commonly misidentified lines
(See ICLAC register)

No commonly misidentified cell lines were used.

Human research participants

Policy information about studies involving human research participants

Population characteristics

The study population was comprised of adults and children who visited either a Kaiser Permanente hospital or Stanford Hopital and were either PCR+ for SARS-CoV-2 or were seropositive by ELISA for SARS-CoV-2 antigens (pediatric samples)

Recruitment

Samples were either remainder sera from clinical laboratories or were recruited under Stanford IRB #NCT04331899 or #29992 or the IRB of Rockefeller University (protocol #TWA-0804)

Ethics oversight

Studies were performed in compliance with the Declaration of Helsinki. Characterization of samples was performed under a protocol approved by the Institutional Review Board of Stanford University (protocol #55718)

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Flow Cytometry

Plots

Confirm that:

☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☒ All plots are contour plots with outliers or pseudocolor plots.

☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation

1-NK cell degranulation
PBMCs were isolated from whole blood collected from healthy blood donors post-plateletpheresis (Stanford Blood Center) using SepMate Isolation Tubes (STEMCELL). PBMCs were plated in a 96-well round-bottom plate (CELLSTAR) at a density of 3 ⍰106 cells/mL of complete RPMI-1640 media supplemented with 1X penicillin-streptomycin-glutamine, 1mM sodium pyruvate, and 1X MEM Non-Essential Amino Acids, 10% heat-inactivated fetal bovine serum (Gibco), and 1ng/mL IL-15 (STEMCELL). Cells were rested overnight at 37⍰C in a 5% CO2 incubator (Panasonic). The following morning, cell culture media was replaced with complete RPMI containing anti-CD107a antibody (BioLegend; clone H4A3). PBMCs were promptly

stimulated for 6hr at 37°C with immune complexes formed by incubating purified patient IgG with SARS-CoV-2 receptor-binding domain protein at a molar ratio of 30:1 for 1hr at room temperature. 1hr into stimulation, culture media was supplemented with 1X Brefeldin A (BioLegend) for the remaining 5hr of culture. Cells were then isolated, stained for cell viability using Live/Dead Fixable Staining Kit (Thermo Fisher) as well as CD3 (clone OKT3), CD11c (clone S-HCL-3), CD14 (clone 63D3), CD16 (clone 3G8), CD56 (clone 5.1H11), and HLA-DR (clone L243) surface markers (BioLegend). After staining, cells were fixed and acquired using an Attune NxT flow cytometer (Invitrogen). NK cells were defined as viable CD3- CD14- CD56+ HLA-DR- cells. NK cell degranulation was measured and reported as the percentage of NK cells positive for CD107a.

2) Cytokine assay:
Monocytes were isolated from healthy donor blood (Stanford Blood Center) using RosetteSep Human Monocyte Enrichment Kit (STEMCELL) per manufacturer instructions. Monocytes were cultured at a density of 2×106 cells/mL in RPMI 1640 media supplemented with 1X non-essential amino acids, sodium pyruvate, penicillin-streptomycin-glutamine (Gibco), and 10% fetal bovine serum (GE Healthcare Life Sciences).
Immune complexes were formed by incubating a dilution series of COVID-19 patient IgGs or anti-spike 3022 mAbs to SARS-CoV-2 spike-expressing delta-G-VSV pseudovirus for 1 hour at room temperature.
Monocytes were incubated with the various immune complexes or the pseudovirus only for 18 hours at 37oC in a 5% CO2 incubator. After 18 hours, cell-free supernatants were collected and proinflammatory cytokine concentrations were measured using a LEGENDplex bead array (BioLegend) per manufacturer instructions.

Instrument

Attune NxT flow cytometer

Software

FlowJo v10.6.2

Cell population abundance

NK cell frequencies within isolated PBMCs ranged from 9-21%

Gating strategy

Single cells were gated on using FSC-A vs FSC-H and SSC-A vs SSC-H gates. Cells smaller than 100k based on FSC-A were excluded. Viable cells were gated on as the negative fraction of cells using Live/Dead Violet Fixable Dead Cell Staining Kit. NK cells were gated on due to their CD56 positivity (>10^3 MFI), CD3/CD14 negativity (<3*10^2 MFI). NK cells were further confirmed as NK cells due to HLA-DR negativity (<10^3 MFI). CD107a+ NK cells were positively gated on from a histogram of CD107a expression among NK cells (>5*10^2 MFI)

☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.